SEQUENCE LISTING

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 Vogel, Monique
 Amstutz, Hanspeter

JUL 2 0 2000

<120> POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE

<130> 6816/P63221US0

<140> 09/147,443

<141> 1999-01-21

<150> PCT/EP97/03253

<151> 1997-06-20

<150> EP 96810421.6

<151> 1996-06-24

<160> 64

<170> PatentIn Ver. 2.1

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90

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25

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Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe 75

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378

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Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	
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Leu	Gln	Met	Arg	Ser 85	Leu	Ser	Ala	Asp	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Arg	Asp	Lys 100	Ala	Val	Arg	Gly	Ile 105	Ser	Arg	Tyr	Asn	Tyr 110	Tyr	Met	
Asp	Val	Trp 115	Gly	Lys	Gly	Thr	Thr 120	Val	Thr	Val	Ser	Ser 125				
<213 <213	0 > 2° 1 > 3° 2 > Di 3 > Ho	L2 NA	sapie	ens												
	0> 1> CI 2> (1		(312))												
gtg	0> 27 atg Met	acc														48
	acc Thr															96
	tat Tyr															144
	tcc Ser 50															192

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ttt gca Phe Ala															288
caa ggg Gln Gly	-	_		_											312
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Val Thi	: Ile	Thr 20	Cys	Arg	Thr	Ser	Gln 25	Thr	Ile	Ser	Arg	Asn 30	Leu	Asn	
Trp Tyr	Gln 35	Gln	Lys	Pro	Gly	Lys 40	Ala	Pro	Lys	Leu	Leu 45	Ile	Tyr	Ala	
Thr Ser		Leu	Gln	Ser	Gly 55	Val	Pro	Ser	Arg	Phe 60	Ser	Gly	Ser	Gly	
Ser Gly 65	Thr	Asp	Phe	Thr 70	Leu	Thr	Ile	Asn	Ser 75	Leu	Gln	Pro	Glu	Asp 80	
Phe Ala	Thr	Tyr	Tyr 85	Cys	Gln	Gln	Ser	Tyr 90	Thr	Thr	Pro	Ser	Phe 95	Gly	
Gln Gly	Thr	Lys 100	Val	Glu	Ile	Lys									
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Ser Leu Arg	ctc tcc Leu Ser 20												96
ggc atg cac Gly Met His 35													144
gct ttt ata Ala Phe Ile 50													192
aag ggc cga Lys Gly Arg 65				_	_			_		-			240
ctg caa atg Leu Gln Met													288
gcg aga gag Ala Arg Glu													336
gac gtc tgg Asp Val Trp 115													375
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<211> 125 <212> PRT <213> Homo s <400> 30 Gln Val Lys	Leu Leu 5			_		10					15	_	
<211> 125 <212> PRT <213> Homo s <400> 30 Gln Val Lys 1	Leu Leu 5 Leu Ser 20	Cys	Val	Ala	Ser 25	10 Gly	Phe	Thr	Phe	Arg 30	15 Ser	Tyr	
<211> 125 <212> PRT <213> Homo s <400> 30 Gln Val Lys 1 Ser Leu Arg	Leu Leu 5 Leu Ser 20 Trp Val	Cys Arg	Val Gln	Ala Ala 40	Ser 25 Pro	Gly	Phe Lys	Thr Gly	Phe Leu 45	Arg 30 Glu	15 Ser Trp	Tyr Val	
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<211> 125 <212> PRT <213> Homo s <400> 30 Gln Val Lys 1 Ser Leu Arg Gly Met His 35 Ala Phe Ile 50 Lys Gly Arg	Leu Leu 5 Leu Ser 20 Trp Val Trp Phe Phe Thr	Cys Arg Asp Ile 70	Val Gln Gly 55 Ser	Ala Ala 40 Ser	Ser 25 Pro Asn Asp	Gly Gly Lys Asn	Phe Lys Gly Ser 75	Thr Gly Tyr 60 Lys	Phe Leu 45 Val Asn	Arg 30 Glu Asp Met	15 Ser Trp Ser Leu	Tyr Val Val Tyr 80	
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gtc acc atc act tgc cgg gca agt cag agc gtt acc agg tct tta aat 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 20 25 30	
tgg tat cag cag aaa cca ggg aaa gcc cct agg ctc cta atc ttt gct 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 35 40 45	4
gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 193 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	2
tct ggg aca gat ttc acc ctc acc atc agc agt ctg caa cct gag gat 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80	0
ttt gga act tac tac tgt caa cag aat tac agg acc cct cag tgg acg 289 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 85 90 95	8
ttc ggc caa ggg acc aag gta gaa atc aaa Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105	8
<210> 32 <211> 106 <212> PRT <213> Homo sapiens	
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Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 35 40 45	
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 90 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys <210> 33 <211> 378 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(378) <400> 33 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 144 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tat 288 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr 85 90 tgt gcg aga gag aag gcg ctt cgg gga atc agc aga tac aac tat tac 336 Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr 105 100 378 ctg gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120

21

<210> 34 <211> 126

<212> PRT

<213> Homo sapiens

<400> 34

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr 85 90 95

Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
100 105 110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

<210> 35

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(333)

<400> 35

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Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
1 5 10 15

act ctc acc tgt gct tcc agc act ggg gca gtc acc agg ggt tac tat 96
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr
20 25 30

cca aac tgg ttc cag cag aag cct gga caa gca ccc agg gca ctg att 144
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile
35 40 45

tat agt aca aac aaa aaa cac tcc tgg acc cct gcc cgg ttc tca ggc 192
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
50 55 60

tcc ctc ctt ggg ggc aaa gct gcc ctg aca ctg tca ggt gtg cag cct 240 Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 65 70 75 80

gaa gac gag go Glu Asp Glu A											288
ctc gta ttc go Leu Val Phe Gi	y Gly G										333
<210> 36 <211> 111 <212> PRT <213> Homo sap	oiens										
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Thr Leu Thr Cy	rs Ala Se 10	er Ser Tl	hr Gly 25	Ala	Val	Thr	Arg	Gly 30	Tyr	Tyr	
Pro Asn Trp Ph 35	e Gln G	_	ro Gly 40	Gln	Ala	Pro	Arg 45	Ala	Leu	Ile	
Tyr Ser Thr As	n Lys Ly	rs His Se 55	er Trp	Thr	Pro	Ala 60	Arg	Phe	Ser	Gly	
Ser Leu Leu Gl 65		s Ala Ai	la Leu	Thr	Leu 75	Ser	Gly	Val	Gln	Pro 80	
Glu Asp Glu A	a Glu Ty 85	r Tyr Cy	ys Leu	Leu 90	Tyr	Tyr	Gly	Gly	Ala 95	Gln	
Leu Val Phe Gl		y Thr Ly	ys Leu 105	Thr	Val	Leu	Arg	Gln 110	Pro		
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tcc ctg aga ct Ser Leu Arg Le											96

Gly Met His 35	tgg gtc Trp Val					ı Glu			14
gca ctt ata Ala Leu Ile 50			_		_	_			92
aag ggc cga Lys Gly Arg 65					c Lys Ası				ŧ 0
ctc caa atg Leu Gln Met				-		•		_	88
gcg aga gac Ala Arg Asp				Ser Arg				_	86
gac gtc tgg (Asp Val Trp (115						-		37	75
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<400> 38 Gln Val Lys 1 1 Ser Leu Arg 1 Gly Met His 3	Leu Leu 5 5 Leu Ser 9 20 Trp Val 2	Cys Glu Arg Gln	Ala Ser 25 Ala Pro 40	10 Gly Phe Gly Lys	e Thr Leu G Gly Leu 45	a Arg 30 a Glu	15 Ser Trp	Ser Val	
<pre><400> 38 Gln Val Lys 1 1 Ser Leu Arg 1 Gly Met His 3 35 Ala Leu Ile 3</pre>	Leu Leu 5 Leu Ser 9 20 Trp Val 2	Cys Glu Arg Gln Asp Gly 55	Ala Ser 25 Ala Pro 40 Ser Ile	Gly Phe Gly Lys Arg Ser	Gly Let 45 Tyr Ala 60 Lys Asr	Arg 30 Glu Glu	15 Ser Trp Ser	Ser Val Val	
<pre><400> 38 Gln Val Lys 1 1 Ser Leu Arg 1 Gly Met His 3 35 Ala Leu Ile 3 50 Lys Gly Arg 1</pre>	Leu Leu 5 Leu Ser 20 Trp Val 2 Trp Phe 2	Cys Glu Arg Gln Asp Gly 55 Ile Ser	Ala Ser 25 Ala Pro 40 Ser Ile Arg Asp	Gly Lys Arg Ser Thr Ser	Thr Let Gly Let 45 Tyr Ala 60 Lys Asr	Arg 30 Glu Glu Thr	15 Ser Trp Ser	Ser Val Val Tyr 80	
<pre><400> 38 Gln Val Lys 1 1 Ser Leu Arg 1 Gly Met His 3 35 Ala Leu Ile 3 50 Lys Gly Arg 1 65 Leu Gln Met A Ala Arg Asp 1</pre>	Leu Leu 5 Leu Ser 2 Trp Val 2 Trp Phe 2 Phe Thr 3	Cys Glu Arg Gln Asp Gly 55 Ile Ser 70 Leu Ser	Ala Ser 25 Ala Pro 40 Ser Ile Arg Asp	Gly Lys Arg Ser Thr Ser 75 Asp Thr 90	Thr Leu Gly Leu 45 Tyr Ala 60 Lys Asr	Arg 30 Glu Glu Thr	15 Ser Trp Ser Leu Tyr 95	Ser Val Val Tyr 80 Cys	

<210> 39 <211> 315 <212> DNA <213> Homo sapiens			
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gtc acc atc act tgc of Val Thr Ile Thr Cys A			
tgg tat cag cac aaa c Trp Tyr Gln His Lys I 35		_	_
gta tcc gct ttg caa a Val Ser Ala Leu Gln S 50			
tct ggg aca gat ttc a Ser Gly Thr Asp Phe 7 65			
ttt gca act tac tac t Phe Ala Thr Tyr Tyr 0 85	Cys Gln Gln Ser Ty		
ggc cag ggg acc aac c Gly Gln Gly Thr Asn I 100			315
<210> 40 <211> 105 <212> PRT <213> Homo sapiens			
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Val Thr Ile Thr Cys A	Arg Ala Ser Gln As 25	sn Ile Gly Ser Tyr 30	Leu Asn
Trp Tyr Gln His Lys I	Pro Gly Thr Ala Pr 40	ro Lys Leu Leu Ile 45	Tyr Ala
Val Ser Ala Leu Gln S	Ser Gly Val Pro Se 55	er Arg Phe Ser Gly 60	Ser Arg

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

26

	65	Cij		пор	11.0	70	200				75					80	
	Phe	Ala	Thr	Tyr	Tyr 85	Cys	Gln	Gln	Ser	Tyr 90	Ser	Pro	Pro	Tyr	Thr 95	Phe	
	Gly	Gln	Gly	Thr 100	Asn	Leu	Gln	Ile	Lys 105								
	<211 <212	0> 41 L> 37 2> DI B> Ho	75 NA	sapie	ens												
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										gga Gly							96
										ggc Gly							144
	_					_	_	_		aaa Lys				_		_	192
	_		_			_		_	_	aat Asn		_		_			240
	-		_			_	_	_	_	gac Asp 90	_	_	_			_	288
										agt Ser							336
										acc Thr							375
)> 42 .> 12															

<211> 125 <212> PRT

<213> Homo sapiens

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ttt gca act tac tac tgt caa cag agt tac agt acc ctg tgg acg ttc Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe ggc caa ggg acc aag gtg gaa atc aaa 315 Gly Gln Gly Thr Lys Val Glu Ile Lys 100 <210> 44 <211> 105 <212> PRT <213> Homo sapiens <400> 44 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys <210> 45 <211> 375 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(375) cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 10 tee etg aga etc tee tgt gta geg tet gga tte ace tte agg agt tat 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40

Ala	ttt Phe 50	Ile	tgg Trp	ttt Phe	gat Asp	gga Gly 55	Ser	aat Asn	aaa Lys	gga Gly	tat Tyr 60	Val	gac Asp	tco Ser	gtg Val	192
aag Lys 65	Gly	cga Arg	ttc Phe	acc Thr	atc Ile 70	tcc Ser	cga Arg	gac Asp	aat Asn	tcc Ser 75	Lys	aac Asn	acg Thr	cto Leu	tat Tyr 80	240
ctg Leu	caa Gln	atg Met	aag Lys	agc Ser 85	ctg Leu	aga Arg	gcc Ala	gag Glu	gac Asp 90	acg Thr	gct Ala	gta Val	tat Tyr	tat Tyr 95	tgt Cys	288
gcg Ala	aga Arg	gag Glu	aag Lys 100	gcg Ala	ctt Leu	cgg Arg	gga Gly	atc Ile 105	agt Ser	aga Arg	tac Tyr	aac Asn	tat Tyr 110	tac Tyr	ctg Leu	336
		tgg Trp 115														375
<21 <21	0 > 4 : 1 > 1: 2 > P: 3 > Ho	25	sapie	ens												
	0> 40	5														
Gln 1	_	Lys	Leu	Leu 5	Glu	Ser	Gly	Gly	Gly 10	Val	Val	Gln	Pro	Gly 15	Gly	
1	Val	_		5					10					15		
1 Ser	Val Leu	Lys	Leu 20	5 Ser	Cys	Val	Ala	Ser 25	10 Gly	Phe	Thr	Phe	Arg 30	15 Ser	Tyr	
Ser Gly	Val Leu Met	Lys Arg His	Leu 20 Trp	5 Ser Val	Cys Arg	Val Gln	Ala Ala 40	Ser 25 Pro	10 Gly Gly	Phe Lys	Thr Gly	Phe Leu 45	Arg 30 Glu	15 Ser Trp	Tyr Val	
Ser Gly	Val Leu Met Phe 50	Lys Arg His	Leu 20 Trp	5 Ser Val Phe	Cys Arg Asp	Val Gln Gly 55	Ala Ala 40 Ser	Ser 25 Pro Asn	Gly Gly Lys	Phe Lys Gly	Thr Gly Tyr 60	Phe Leu 45 Val	Arg 30 Glu Asp	15 Ser Trp Ser	Tyr Val	
Ser Gly Ala Lys 65	Val Leu Met Phe 50 Gly	Lys Arg His 35	Leu 20 Trp Trp	5 Ser Val Phe Thr	Cys Arg Asp Ile 70	Val Gln Gly 55 Ser	Ala Ala 40 Ser Arg	Ser 25 Pro Asn Asp	Gly Gly Lys Asn	Phe Lys Gly Ser 75	Thr Gly Tyr 60 Lys	Phe Leu 45 Val Asn	Arg 30 Glu Asp	15 Ser Trp Ser Leu	Tyr Val Val Tyr 80	
Ser Gly Ala Lys 65 Leu	Val Leu Met Phe 50 Gly Gln	Lys Arg His 35 Ile Arg Met	Leu 20 Trp Trp Phe	Ser Val Phe Thr Ser 85	Cys Arg Asp Ile 70 Leu	Val Gln Gly 55 Ser	Ala Ala 40 Ser Arg Ala	Ser 25 Pro Asn Asp	Gly Gly Lys Asn Asp 90	Phe Lys Gly Ser 75 Thr	Thr Gly Tyr 60 Lys	Phe Leu 45 Val Asn	Arg 30 Glu Asp Thr	15 Ser Trp Ser Leu	Tyr Val Val Tyr 80 Cys	

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<213> Homo sapiens

<220> <221> CDS <222> (1)(315)														
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tgg tat cag cag aaa cca ggg aca gcc cct aag ctc ctg atc tat gct Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45	144													
gca tcc agg ttg caa agt ggg gtc cca tca agg ttc agt ggc agt ggg Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	192													
tct ggg aca gat ttc act ctc acc atc agc act ctg caa cct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80	240													
ttt gcg act tac tac tgt caa cag agt tac agt gcc cct tgg acg ttc Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95	288													
ggc caa ggg acc aag ctg gaa atc aaa Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105	315													
<210> 48 <211> 105 <212> PRT <213> Homo sapiens														
<pre><400> 48 Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15</pre>														
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30														
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45														
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60														
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80														
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95														

Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105

<212 <212	<210> 49 <211> 375 <212> DNA <213> Homo sapiens															
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					gag Glu											48
					tgt Cys											96
					cgc Arg											144
_					gat Asp		_					_	_			192
					atc Ile 70											240
					ctg Leu											288
	_		_		ctt Leu				_	_					_	336
					ggg ggg											375
<212 <212	0> 50 L> 12 2> PF B> Ho	25	sapie	ens												
)> 5(Val		Leu	Leu 5	Glu	Ser	Gly	Gly	Gly 10	Val	Val	Gln	Pro	Gly 15	Gly	

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Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 <210> 51 <211> 315 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(315) <400> 51 gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg gtc acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 40 gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 55 tot ggg aca gat tto act cto acc atc agc agt ctg caa cot gaa gat 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 70 ttt gca act tac tac tgt caa cag agt tac agt acc cga ttc act ttc 288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe

90

85

315

ggc cct ggg acc aaa gtg gat atc aaa

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cta Leu	caa Gln	atg Met	aac Asn	agc Ser 85	ctg Leu	aga Arg	gtc Val	gag Glu	gac Asp 90	acg Thr	gct Ala	gtg Val	tat Tyr	tac Tyr 95	tgt Cys
gcg Ala	agg Arg	gat Asp	tac Tyr 100	tat Tyr	agc Ser	gtt Val	act Thr	aag Lys 105	aaa Lys	ctc Leu	aga Arg	ctc Leu	cac His 110	tac Tyr	tac Tyr
tac Tyr	tac Tyr	atg Met 115	gac Asp	gtc Val	tgg Trp	ggc Gly	aaa Lys 120	Gly aaa	acc Thr	acg Thr	gtc Val	acc Thr 125	gtc Val	tcc Ser	tca Ser
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Ala	Asp 50	Ile	Trp	Phe	Asp	Gly 55	Gly	Asn	Lys	His	Tyr 60	Ala	Asp	Phe	Val
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Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Val	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Asp	Tyr 100	Tyr	Ser	Val	Thr	Lys 105	Lys	Leu	Arg	Leu	His 110	Tyr	Tyr
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gtc Val	acc Thr	ato Ile	act Thr 20	Cys	cgg Arg	gca Ala	agt Ser	cag Gln 25	Gly	att Ile	aga Arg	aat JAsn	gat Asp 30	Leu	acc Thr	96
tgg Trp	tat Tyr	cag Gln 35	Gln	aaa Lys	cca Pro	ggg Gly	aaa Lys 40	Ala	cct Pro	aag Lys	ctc Leu	ctg Leu 45	Ile	tat Tyr	gct Ala	144
gca Ala	tcc Ser 50	aat Asn	tta Leu	caa Gln	agt Ser	999 55	gtc Val	cca Pro	tca Ser	agg Arg	ttc Phe 60	Ser	ggc	agt Ser	gga Gly	192
tct Ser 65	ggc Gly	aca Thr	gat Asp	ttc Phe	act Thr 70	ctc Leu	acc Thr	atc Ile	agc Ser	agc Ser 75	ctg Leu	cag Gln	cct Pro	gaa Glu	gat Asp 80	240
ttt Phe	gca Ala	act Thr	tat Tyr	tac Tyr 85	tgt Cys	cta Leu	caa Gln	gat Asp	aac Asn 90	aat Asn	ttc Phe	ccg Pro	tac Tyr	act Thr 95	ttt Phe	288
ggc Gly	cag Gln	gly aaa	acc Thr 100	aag Lys	ctg Leu	gag Glu	atc Ile	aaa Lys 105								315
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Val			20					25					30			
Trp '	Tyr	Gln 35	Gln	Lys	Pro	Gly	Lys 40	Ala	Pro	Lys	Leu	Leu 45	Ile	Tyr	Ala	
Ala	Ser 50	Asn	Leu	Gln	Ser	Gly 55	Val	Pro	Ser	Arg	Phe 60	Ser	Gly	Ser	Gly	
Ser (Gly	Thr	Asp	Phe	Thr 70	Leu	Thr	Ile	Ser	Ser 75	Leu	Gln	Pro	Glu	Asp 80	
Phe A	Ala '	Thr	Tyr	Tyr 85	Cys	Leu	Gln	Asp	Asn 90	Asn	Phe	Pro	Tyr	Thr 95	Phe	
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Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
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ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt
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Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
                          55
aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat
                                                                    240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
                      70
ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt
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Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg
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Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
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                                 105
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 55 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 <210> 59 <211> 315 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(315) <400> 59 gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat act Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr 35 gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 50 tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe ggc cag ggg acc aag ctg cag atc aaa 315 Gly Gln Gly Thr Lys Leu Gln Ile Lys 100

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50

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ctg caa atg Leu Gln Met	g aac gge : Asn Gly 8!	y Leu Ar	a gcc g Ala	gaa Glu	gac Asp 90	acg Thr	gct Ala	gta Val	tat Tyr	tat Tyr 95	tgt Cys	288
gcg aga gag Ala Arg Glu	aag gcg Lys Ala 100	g gtt cg a Val Ar	g gga g Gly	att Ile 105	agt Ser	aga Arg	tac Tyr	aac Asn	tac Tyr 110	tac Tyr	atg Met	336
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Gly Met His 35	Trp Val	Arg Glr	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
Ala Phe Ile 50	Trp Phe	Asp Ala		Asn	Lys	Gly	Tyr 60	Gly	Asp	Ser	Val	
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Leu Gln Met	Asn Gly 85	Leu Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala Arg Glu	Lys Ala 100	Val Arg		Ile 105	Ser	Arg	Tyr		Tyr 110	Tyr	Met	
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gtc Val	acc Thr	atc Ile	act Thr	Cys	cgg Arg	gca Ala	agt Ser	cag Gln 25	Ser	att Ile	ato E Ile	aga Arg	tat Tyr 30	tta Leu	aat Asn	96
tgg Trp	tat Tyr	cag Gln 35	His	aaa Lys	cca Pro	Gly 999	aaa Lys 40	Ala	cct Pro	aag Lys	g cto s Leu	ctg Leu 45	Ile	cat His	gct Ala	144
gca Ala	tcc Ser 50	agt Ser	ttg Leu	caa Gln	agt Ser	999 Gly 55	gtc Val	ccg Pro	tca Ser	agg Arg	ttc Phe 60	Ser	ggc	agt Ser	gta Val	192
tct Ser 65	gly ggg	aca Thr	gat Asp	ttc Phe	act Thr 70	ctc Leu	acc Thr	atc Ile	agc Ser	agt Ser 75	Leu	caa Gln	cct Pro	gaa Glu	gat Asp 80	240
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ggc Gly	cag Gln	gly ggg	acc Thr 100	aag Lys	ctg Leu	cag Gln	atc Ile	aaa Lys 105								315
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Trp	Tyr (Gln 35	His	Lys	Pro	Gly	Lys 40	Ala	Pro	Lys	Leu	Leu 45	Ile	His	Ala	
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Ser (Gly T	Thr .	Asp	Phe	Thr 70	Leu '	Thr	Ile	Ser	Ser 75	Leu	Gln	Pro	Glu i	Asp 80	
Phe A	Ala T	Thr '	Tyr	Tyr 85	Cys	Gln (Gln	Ser	Tyr 90	Thr	Thr	Pro	Tyr	Thr 1	Phe	
Gly (3ln G		Thr :	Lys :	Leu (Gln :		Lys 105								